

0570  
0725



RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/887,853

DATE: 07/30/2002

TIME: 14:22:01

Input Set : N:\CrF3\RULE60\09887853.raw  
Output Set: N:\CRF3\07302002\I887853.raw

## SEQUENCE LISTING

3 (1) GENERAL INFORMATION:  
4 (i) APPLICANT: Huston, James S.  
5 Oppermann, Hermann  
6 Houston, L. L.  
7 Ring, David B.  
8  
9 (ii) TITLE OF INVENTION: Biosynthetic Binding Proteins For  
10 Imaging  
11  
12 (iii) NUMBER OF SEQUENCES: 11  
13  
14 (iv) CORRESPONDENCE ADDRESS:  
15 (A) ADDRESSEE: Testa, Hurwitz & Thibeault/Patent Department  
16 (B) STREET: Exchange Place, 53 State Street  
17 (C) CITY: Boston  
18 (D) STATE: Massachusetts  
19 (E) COUNTRY: USA  
20 (F) ZIP: 02109  
21  
22 (v) COMPUTER READABLE FORM:  
23 (A) MEDIUM TYPE: Floppy disk  
24 (B) COMPUTER: IBM PC compatible  
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25  
27  
28 (vi) CURRENT APPLICATION DATA:  
29 (A) APPLICATION NUMBER: US/09/887,853  
30 (B) FILING DATE: 21-Jun-2001  
31 (C) CLASSIFICATION:  
32  
33 (vii) PRIOR APPLICATION DATA:  
34 (A) APPLICATION NUMBER: US/08/133,804  
35 (B) FILING DATE:  
36  
37 (viii) ATTORNEY/AGENT INFORMATION:  
38 (A) NAME: Kelley, Robin D.  
39 (B) REGISTRATION NUMBER: 34,637  
40 (C) REFERENCE/DOCKET NUMBER: 2054/22  
41  
42 (ix) TELECOMMUNICATION INFORMATION:  
43 (A) TELEPHONE: 617-248-7477  
44 (B) TELEFAX: 617-248-7100  
45  
46 (2) INFORMATION FOR SEQ ID NO: 1:  
47 (i) SEQUENCE CHARACTERISTICS:  
48 (A) LENGTH: 909 base pairs  
49 (B) TYPE: nucleic acid  
50 (C) STRANDEDNESS: single  
51 (D) TOPOLOGY: linear  
52  
53 (ii) MOLECULE TYPE: cDNA  
54  
55 (ix) FEATURE:  
56  
57  
58  
59  
60  
61  
62  
63

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Input Set : N:\Crf3\RULE60\09887853.raw  
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64 (A) NAME/KEY: CDS  
 65 (B) LOCATION: 3..752  
 66 (D) OTHER INFORMATION: /product= "741F8 sFv' C-terminal  
 67 Gly4-Cys"  
 70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 72 CC ATG GCG GAG ATC CAA TTG GTG CAG TCT GGA CCT GAG CTG AAG AAG 47  
 73 Met Ala Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys  
 74 1 5 10 15  
 76 CCT GGA GAG ACA GTC AAG ATC TCC TGC AAG GCT TCT GGG TAT ACC TTC 95  
 77 Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 78 20 25 30  
 80 ACA AAC TAT GGA ATG AAC TGG GTG AAG CAG GCT CCA GGA AAG GGT TTA 143  
 81 Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu  
 82 35 40 45  
 84 AAG TGG ATG GGC TGG ATA AAC ACC AAC ACT GGA GAG CCA ACA TAT GCT 191  
 85 Lys Trp Met Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala  
 86 50 55 60  
 88 GAA GAG TTC AAG GGA CGG TTT GCC TTC TCT TTG GAA ACC TCT GCC AGC 239  
 89 Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser  
 90 65 70 75  
 92 ACT GCC TAT TTG CAG ATC AAC AAC CTC AAA AAT GAG GAC ACG GCT ACA 287  
 93 Thr Ala Tyr Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr  
 94 80 85 90 95  
 96 TAT TTC TGT GGA AGG CAA TTT ATT ACC TAC GGC GGG TTT GCT AAC TGG 335  
 97 Tyr Phe Cys Gly Arg Gln Phe Ile Thr Tyr Gly Gly Phe Ala Asn Trp  
 98 100 105 110  
 100 GGC CAA GGG ACT CTG GTC ACT GTC TCT GCA TCG AGC TCC TCC GGA TCT 383  
 101 Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ser Ser Ser Ser Gly Ser  
 102 115 120 125  
 104 TCA TCT AGC GGT TCC AGC TCG AGC GAT ATC GTC ATG ACC CAG TCT CCT 431  
 105 Ser Ser Ser Gly Ser Ser Ser Asp Ile Val Met Thr Gln Ser Pro  
 106 130 135 140  
 108 AAA TTC ATG TCC ACG TCA GTG GGA GAC AGG GTC AGC ATC TCC TGC AAG 479  
 109 Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Ser Cys Lys  
 110 145 150 155  
 112 GCC AGT CAG GAT GTG AGT ACT GCT GTA GCC TGG TAT CAA CAA AAA CCA 527  
 113 Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro  
 114 160 165 170 175  
 116 GGG CAA TCT CCT AAA CTA CTG ATT TAC TGG ACA TCC ACC CGG CAC ACT 575  
 117 Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr  
 118 180 185 190  
 120 GGA GTC CCT GAT CGC TTC ACA GGC AGT GGA TCT GGG ACA GAT TAT ACT 623  
 121 Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Tyr Thr  
 122 195 200 205  
 124 CTC ACC ATC AGC AGT GTG CAG GCT GAA GAC CTG GCA CTT CAT TAC TGT 671  
 125 Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu His Tyr Cys  
 126 210 215 220  
 128 CAG CAA CAT TAT AGA GTG CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG 719  
 129 Gln Gln His Tyr Arg Val Pro Tyr Thr Phe Gly Gly Thr Lys Leu

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130	225	230	235													
132	GAG	ATA	AAA	CGG	GCT	GAT	GGG	GGA	GGT	GGA	TGT	TAACGGGGGA	GGTGGATGTT	772		
133	Glu	Ile	Lys	Arg	Ala	Asp	Gly	Gly	Gly	Cys						
134	240				245				250							
136	GGGTCTCGTT	ACGTTGCGGA	TCTCGAGGCT	ATCTTTACTA	ACTCTTACCG	TAAAGTTCTG							832			
138	GCTCAACTGT	CTGCACGCAA	GCTTTGCAG	GATATCATGA	GCGCTTAAGA	TCCGTCGACC							892			
140	TGCAGGCATG	CAAGCTT											909			
143	(2)	INFORMATION FOR SEQ ID NO: 2:														
145	(i)	SEQUENCE CHARACTERISTICS:														
146	(A)	LENGTH: 250 amino acids														
147	(B)	TYPE: amino acid														
148	(D)	TOPOLOGY: linear														
150	(ii)	MOLECULE TYPE: protein														
152	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 2:														
154	Met	Ala	Glu	Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu	Leu	Lys	Pro	
155	1				5				10				15			
157	Gly	Glu	Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr
158					20				25				30			
160	Asn	Tyr	Gly	Met	Asn	Trp	Val	Lys	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Lys
161					35				40				45			
163	Trp	Met	Gly	Trp	Ile	Asn	Thr	Asn	Thr	Gly	Glu	Pro	Thr	Tyr	Ala	Glu
164					50				55				60			
166	Glu	Phe	Lys	Gly	Arg	Phe	Ala	Phe	Ser	Leu	Glu	Thr	Ser	Ala	Ser	Thr
167					65				70				75			80
169	Ala	Tyr	Leu	Gln	Ile	Asn	Asn	Leu	Lys	Asn	Glu	Asp	Thr	Ala	Thr	Tyr
170					85				90				95			
172	Phe	Cys	Gly	Arg	Gln	Phe	Ile	Thr	Tyr	Gly	Gly	Phe	Ala	Asn	Trp	Gly
173					100				105				110			
175	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala	Ser	Ser	Ser	Ser	Gly	Ser	Ser
176					115				120				125			
178	Ser	Ser	Gly	Ser	Ser	Ser	Ser	Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Lys
179					130				135				140			
181	Phe	Met	Ser	Thr	Ser	Val	Gly	Asp	Arg	Val	Ser	Ile	Ser	Cys	Lys	Ala
182					145				150				155			160
184	Ser	Gln	Asp	Val	Ser	Thr	Ala	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly
185					165				170				175			
187	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Thr	Ser	Thr	Arg	His	Thr	Gly
188					180				185				190			
190	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Leu
191					195				200				205			
193	Thr	Ile	Ser	Ser	Val	Gln	Ala	Glu	Asp	Leu	Ala	Leu	His	Tyr	Cys	Gln
194					210				215				220			
196	Gln	His	Tyr	Arg	Val	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu
197					225				230				235			240
199	Ile	Lys	Arg	Ala	Asp	Gly	Gly	Gly	Cys							
200					245				250							
202	(2)	INFORMATION FOR SEQ ID NO: 3:														
204	(i)	SEQUENCE CHARACTERISTICS:														
205	(A)	LENGTH: 779 base pairs														

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206 (B) TYPE: nucleic acid  
207 (C) STRANDEDNESS: single  
208 (D) TOPOLOGY: linear  
210 (ii) MOLECULE TYPE: cDNA  
213 (ix) FEATURE:  
214 (A) NAME/KEY: CDS  
215 (B) LOCATION: 3..758  
216 (D) OTHER INFORMATION: /product= "26-10 sFv' with  
217 C-terminal Gly4-Cys"  
220 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
222 CC ATG GAA GTT CAA CTG CAA CAG TCT GGT CCT GAA TTG GTT AAA CCT 47  
223 Met Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro  
224 1 5 10 15  
226 GGC GCC TCT GTG CGC ATG TCC TGC AAA TCC TCT GGG TAC ATT TTC ACC 95  
227 Gly Ala Ser Val Arg Met Ser Cys Lys Ser Ser Gly Tyr Ile Phe Thr  
228 20 25 30  
230 GAC TTC TAC ATG AAT TGG GTT CGC CAG TCT CAT GGT AAG TCT CTA GAC 143  
231 Asp Phe Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Asp  
232 35 40 45  
234 TAC ATC GGG TAC ATT TCC CCA TAC TCT GGG GTT ACC GGC TAC AAC CAG 191  
235 Tyr Ile Gly Tyr Ile Ser Pro Tyr Ser Gly Val Thr Gly Tyr Asn Gln  
236 50 55 60  
238 AAG TTT AAA GGT AAG GCG ACC CTT ACT GTC GAC AAA TCT TCC TCA ACT 239  
239 Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr  
240 65 70 75  
242 GCT TAC ATG GAG CTG CGT TCT TTG ACC TCT GAG GAC TCC GCG GTA TAC 287  
243 Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr  
244 80 85 90 95  
246 TAT TGC GCG GGC TCC TCT GGT AAC AAA TGG GCC ATG GAT TAT TGG GGT 335  
247 Tyr Cys Ala Gly Ser Ser Gly Asn Lys Trp Ala Met Asp Tyr Trp Gly  
248 100 105 110  
250 CAT GGT GCT AGC GTT ACT GTG AGC TCC TCC GGA TCT TCA TCT AGC GGT 383  
251 His Gly Ala Ser Val Thr Val Ser Ser Ser Gly Ser Ser Ser Gly  
252 115 120 125  
254 TCC AGC TCG AGT GGA TCC GAC GTC GTA ATG ACC CAG ACT CCG CTG TCT 431  
255 Ser Ser Ser Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser  
256 130 135 140  
258 CTG CCG GTT TCT CTG GGT GAC CAG GCT TCT ATT TCT TGC CGC TCT TCC 479  
259 Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser  
260 145 150 155  
262 CAG TCT CTG GTC CAT TCT AAT GGT AAC ACT TAC CTG AAC TGG TAC CTG 527  
263 Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Leu  
264 160 165 170 175  
266 CAA AAG GCT GGT CAG TCT CCG AAG CTT CTG ATC TAC AAA GTC TCT AAC 575  
267 Gln Lys Ala Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn  
268 180 185 190  
270 CGC TTC TCT GGT GTC CCG GAT CGT TTC TCT GGT TCT GGT TCT GGT ACT 623  
271 Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr  
272 195 200 205

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274 GAC	TTC	ACC	CTG	AAG	ATC	TCT	CGT	GTC	GAG	GCC	GAA	GAC	CTG	GGT	ATC	671
275 Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Ile	
276	210							215						220		
278 TAC	TTC	TGC	TCT	CAG	ACT	ACT	CAT	GTA	CCG	CCG	ACT	TTT	GGT	GGT	GGC	719
279 Tyr	Phe	Cys	Ser	Gln	Thr	Thr	His	Val	Pro	Pro	Thr	Phe	Gly	Gly	Gly	
280	225							230				235				
282 ACC	AAG	CTC	GAG	ATT	AAA	CGT	TCC	GGG	GGA	GGT	GGA	TGT	TAACTGCAGC		768	
283 Thr	Lys	Leu	Glu	Ile	Lys	Arg	Ser	Gly	Gly	Gly	Gly	Cys				
284	240							245				250				
286 CCGGGGGATC C															779.	
289 (2) INFORMATION FOR SEQ ID NO: 4:																
291 (i) SEQUENCE CHARACTERISTICS:																
292 (A) LENGTH: 252 amino acids																
293 (B) TYPE: amino acid																
294 (D) TOPOLOGY: linear																
296 (ii) MOLECULE TYPE: protein																
298 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:																
300 Met	Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	Lys	Pro	Gly	
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303 Ala	Ser	Val	Arg	Met	Ser	Cys	Lys	Ser	Ser	Gly	Tyr	Ile	Phe	Thr	Asp	
304		20						25						30		
306 Phe	Tyr	Met	Asn	Trp	Val	Arg	Gln	Ser	His	Gly	Lys	Ser	Leu	Asp	Tyr	
307		35						40						45		
309 Ile	Gly	Tyr	Ile	Ser	Pro	Tyr	Ser	Gly	Val	Thr	Gly	Tyr	Asn	Gln	Lys	
310		50						55						60		
312 Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	
313		65				70				75					80	
315 Tyr	Met	Glu	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	
316			85						90					95		
318 Cys	Ala	Gly	Ser	Ser	Gly	Asn	Lys	Trp	Ala	Met	Asp	Tyr	Trp	Gly	His	
319			100					105						110		
321 Gly	Ala	Ser	Val	Thr	Val	Ser	Ser	Gly	Ser	Ser	Ser	Ser	Gly	Ser		
322		115				120								125		
324 Ser	Ser	Ser	Gly	Ser	Asp	Val	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	
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327 Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	
328		145				150				155					160	
330 Ser	Leu	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	Asn	Trp	Tyr	Leu	Gln	
331			165					170						175		
333 Lys	Ala	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	
334			180					185						190		
336 Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	
337		195						200						205		
339 Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Ile	Tyr	
340		210				215					220					
342 Phe	Cys	Ser	Gln	Thr	Thr	His	Val	Pro	Pro	Thr	Phe	Gly	Gly	Gly	Thr	
343		225				230				235					240	
345 Lys	Leu	Glu	Ile	Lys	Arg	Ser	Gly	Gly	Gly	Gly	Cys					
346			245					250								

RAW SEQUENCE LISTING ERROR SUMMARY                    DATE: 07/30/2002  
PATENT APPLICATION: US/09/887,853                    TIME: 14:22:02

Input Set : N:\Crf3\RULE60\09887853.raw  
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

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Seq#:2; Line(s) 202  
Seq#:3; Line(s) 289  
Seq#:4; Line(s) 348  
Seq#:5; Line(s) 433  
Seq#:6; Line(s) 492  
Seq#:7; Line(s) 514  
Seq#:8; Line(s) 536  
Seq#:9; Line(s) 558  
Seq#:10; Line(s) 581

**VERIFICATION SUMMARY**

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Input Set : N:\Crf3\RULE60\09887853.raw  
Output Set: N:\CRF3\07302002\I887853.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]